

enzyme, exhibits increased heat stability relative to the wild type ADP-glucose pyrophosphorylase enzyme.

[Claim 3 (amended):]

3. The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation in the large subunit of said mutant enzyme.

[Claim 4 (amended):]

4. The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation in the small subunit of said mutant enzyme.

[Claim 5 (amended):]

a. 5. The polynucleotide according to claim 3, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 333 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

[Claim 6 (amended):]

6. The polynucleotide according to claim 5, wherein said amino acid substituted for the amino acid corresponding to position 333 is a glycine.

[Claim 7 (amended):]

7. The polynucleotide according to claim 5, wherein said amino acid substituted for the amino acid corresponding to position 333 is a phenylalanine.

[Claim 8 (amended):]

8. The polynucleotide according to claim 5, wherein said amino acid substituted for the amino acid corresponding to position 333 is a methionine.

a2 [Claim 9 (amended):]

9. The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

a3 [Claim 11 (amended):]

11. The polynucleotide according to claim 9, wherein said polynucleotide encodes a large subunit AGP enzyme wherein at least one serine residue is inserted between amino acids corresponding to positions 494 and 495 in the amino acid sequence of wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize of the native AGP enzyme subunit.

a3 [Claim 12 (amended):]

12. The polynucleotide according to claim 9, wherein said polynucleotide encodes a large subunit AGP enzyme wherein the amino acid pair tyrosine:serine is inserted between amino acids corresponding to positions 494 and 495 in the amino acid sequence of wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize of the native AGP enzyme subunit.

[Claim 13 (amended):]

13. The polynucleotide according to claim 9, wherein said polynucleotide encodes a large subunit AGP enzyme wherein the amino acid pair serine:tyrosine is inserted between amino acids corresponding to positions 495 and 496 in the amino acid sequence of wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize of the native AGP enzyme subunit.

a4 [Claim 15 (amended):]

15. The method according to claim 14, wherein said plant is a monocotyledonous plant.

a5 [Claim 27 (amended):]

27. A mutant subunit of a plant ADP-glucose pyrophosphorylase polypeptide, or a biologically-active fragment of said mutant polypeptide, encoded by the polynucleotide of claim 1.

[Claim 28 (amended):]

28. A method for identifying a polynucleotide encoding a mutant subunit of a plant ADP-glucose pyrophosphorylase polypeptide wherein said mutant polypeptide comprises an amino acid mutation in the amino acid sequence of said polypeptide and wherein when said mutant polypeptide is expressed to form a mutant ADP-glucose pyrophosphorylase enzyme, said mutant enzyme, or a biologically-active fragment of said mutant enzyme, exhibits increased heat stability relative to a wild type ADP-glucose pyrophosphorylase enzyme, said method comprising mutating a polynucleotide encoding a starch biosynthesis protein, expressing said mutated polynucleotide in a cell to produce a mutant starch biosynthesis protein, and determining whether said mutant starch biosynthesis protein exhibits increased heat stability relative to the wild type starch biosynthesis protein.

Please add ~~the~~ following new claims 30-41:

30. The polynucleotide according to claim 3, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the histidine amino acid at position 333 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

31. The polynucleotide according to claim 30, wherein said amino acid substituted for histidine at position 333 is a glycine.

32. The polynucleotide according to claim 30, wherein said amino acid substituted for histidine at position 333 is a phenylalanine.

33. The polynucleotide according to claim 30, wherein said amino acid substituted for histidine at position 333 is a methionine.

34. The polynucleotide according to claim 9, wherein said polynucleotide encodes a large subunit AGP enzyme wherein at least one serine residue is inserted between the amino acids at positions 494 and 495 in the amino acid sequence of wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize of the native AGP enzyme subunit.

35. The polynucleotide according to claim 9, wherein said polynucleotide encodes a large subunit AGP enzyme wherein the amino acid pair tyrosine:serine is inserted between the amino acids at positions 494 and 495 in the amino acid sequence of wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize of the native AGP enzyme subunit.

36. The polynucleotide according to claim 9, wherein said polynucleotide encodes a large subunit AGP enzyme wherein the amino acid pair serine:tyrosine is inserted between the amino acids at positions 495 and 496 in the amino acid sequence of wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize of the native AGP enzyme subunit.

37. The polynucleotide according to claim 1, wherein said plant is a monocotyledonous plant.

38. The polynucleotide according to claim 37, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lilies, and millet.

39. The polynucleotide according to claim 1, wherein said plant is *Zea mays*.

40. The polynucleotide according to claim 1, wherein said plant is a dicotyledonous plant.

41. The polynucleotide according to claim 40, wherein said dicotyledonous plant is selected from the group consisting of peas, alfalfa, chickpea, chicory, clover, kale, lentil, prairie grass, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, and lettuce.